



SEQUENCE LISTING

<110> Möckel, Bettina
Pfefferle, Walter

<120> NOVEL NUCLEOTIDE SEQUENCES ENCODING THE GPM GENE

<130> 21123/273989

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 1020

<212> DNA

<213> Corynebacterium glutamicum

<221> CDS

<222> (181)..(924)

<400> 1
acgcgcatca gaatgggtga agacgccgtc gaacacgccca gaacattctc ctggggcggcc 60
accgccgcac agctatcgtc gctgtacaac gacgctattg ccaacgaaaa tgtcgacggc 120
gaaacgcatac acggctaagt aaacgcgcgt cgtggaacat aaagtggcaa actagtagcct 180
atg act aac gga aaa ttg att ctt ctt cgt cac ggt cag agc gaa tgg 228
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
1 5 10 15
aac gca tcc aac cag ttc act gga tgg gtc gac gtc aat ctg acc gaa 276
Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
20 25 30
cag ggt gag gct gag gcc aag cgc gga ggc gaa ctc ctc gtc gag gca 324
Gln Gly Glu Ala Glu Ala Lys Arg Gly Gly Glu Leu Leu Val Glu Ala
35 40 45
ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc gcg atc 372
Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg Ala Ile
50 55 60
cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg atc cca 420
Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp Ile Pro
65 70 75 80
gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca ctg cag 468
Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
85 90 95

ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac cag ttc 516
 Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp Gln Phe
 100 105 110
 atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc gcg gat 564
 Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
 115 120 125
 gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac ctc gac 612
 Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp Leu Asp
 130 135 140
 gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt ttt gtt 660
 Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg Phe Val
 145 150 155 160
 cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc gaa acc 708
 Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly Glu Thr
 165 170 175
 gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt aag cac 756
 Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val Lys His
 180 185 190
 ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc cca acc 804
 Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile Pro Thr
 195 200 205
 ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta gta aac 852
 Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val Val Asn
 210 215 220
 cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc gca gca 900
 Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
 225 230 235 240
 gca gta gca aac cag ggt aat aag tagctatttg taggtgagca ctcttcttg 954
 Ala Val Ala Asn Gln Gly Asn Lys
 245
 tttcgtattg ggctgtgtcc tcatgggcct cgccctacct gcgtatacga aaattaaaga 1014
 tcggat 1020

<210> 2

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2

Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
 1 5 10 15

Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
 20 25 30

Gln Gly Glu Ala Glu Ala Lys Arg Gly Gly Glu Leu Leu Val Glu Ala
 35 40 45

Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg Ala Ile
 50 55 60

Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp Ile Pro
 65 70 75 80

Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
 85 90 95

Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp Gln Phe
 100 105 110

Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
 115 120 125

Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp Leu Asp
 130 135 140

Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg Phe Val
 145 150 155 160

Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly Glu Thr
 165 170 175

Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val Lys His
 180 185 190

Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile Pro Thr
 195 200 205

Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val Val Asn
 210 215 220

Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
 225 230 235 240

Ala Val Ala Asn Gln Gly Asn Lys
 245

<210> 3

<211> 20

<212> DNA

<213> PCR primer

<400> 3
taaagtggca aactagtacc

20

<210> 4

<211> 19

<212> DNA

<213> PCR primer

<400> 4
ctacttatta ccctgggtt

19